REMARKS

Objection for not complying with sequence rules

The Examiner has objected to the specification as requiring the insertion of sequence identifiers in front of sequences referred to in the specification.

Applicants respectfully point out that SEQ ID NOS are included throughout the specification where sequences are referred to, as well as in the figures. For example, SEQ ID NOS are given at the end of the cDNA sequence in Figure 1 (SEQ ID NO:1), at the end of the protein sequence in Figure 2 (SEQ ID NO:2), at the end of the genomic sequence in Figure 3 (SEQ ID NO:3), and at the end of the protein sequences of Genbank gi/10438148 (SEQ ID NO:4) and gi/5802604 (SEQ ID NO:5) in the BLAST alignment in Figure 2. In the specification, SEQ ID NOS are indicated in the Description of the Figures (pages 9-10 of the specification) and throughout the specification where reference is made to transcript/cDNA (SEQ ID NO:1), amino acid (SEQ ID NO:2), or genomic (SEQ ID NO:3) sequences; see, for example, pages 13 and 34-35 of the specification. Amino acid fragments given in Figure 2 are fragments of SEQ ID NO:2; amino acid residue positions are given for these fragments that indicate their position within SEQ ID NO:2. Nucleic acid fragments given in Figure 3 are fragments of SEQ ID NO:3; nucleotide positions are given for the SNPs contained within these fragments that indicate their positions within SEQ ID NO:3.

Objection to discrepancies between cDNA of SEQ ID NO:1 and genomic sequence of SEQ ID NO:3

The Examiner has objected to the specification for having discrepancies between the cDNA of SEQ ID NO:1 and the corresponding exons of the genomic DNA of SEQ ID NO:3.

In response, Applicants have hereby deleted claim element 4(c), which is directed to SEQ ID NO:3, because the protein of SEQ ID NO:2 is encoded by the transcript/cDNA sequence of SEQ ID NO:1 and the minor differences (e.g., substitutions and insertions/deletions) that exist in SEQ ID NO:3 compared with SEQ ID NO:1 may

encode a protein having minor amino acid differences compared with SEQ ID NO:2. However, the genomic sequence of SEQ ID NO:3 is the correct genomic region, which contains the transcript of SEQ ID NO:1 and also provides additional nucleotide sequences flanking SEQ ID NO:1.

Objection to Drawings:

The drawings requirement will be complied with upon the allowance of the presently rejected claims.

Rejection of claim 24 under 35 USC §112 second paragraph

Examiner pointed out that claim 24 is unclear as to the identity of the polypeptide being produced because the host cell of claim 9 is capable of producing a large number of polypeptides, both native and recombinant.

In response, Applicant has hereby amended claim 24 to specifically define the intended polypeptide to be a polypeptide comprising SEQ ID NO:2.

Claim 24 has also been amended to provide proper antecedent basis for "the peptide".

Rejection of claim 4 (and claims 8-9, 13, 24, 27-29, which are dependent thereon) under 35 USC §112 first paragraph

Examiner has rejected claim 4, specifically claim 4(a), (and, consequently, claims 8-9, 13, 24, 27-29, which are dependent thereon) stating that the specification does not disclose any specific coding or non-coding sequences that could be part of the nucleic acid molecule encoding a protein comprising the amino acid sequence of SEQ ID NO:2. While some of these additional coding and non-coding sequences are known in the art, there are many sequences that can be fused to the nucleic acid molecule of claim 4(a) with functions and/or uses that have not been disclosed. Thus, Applicants have not provided sufficient guidance to enable one of ordinary skill in the art to make and use the claimed invention in a manner reasonably correlated with the scope of the claim.

In response, Applicants respectfully assert that the specification does disclose numerous examples of sequences that could be part of a nucleic acid molecule encoding a

protein comprising SEQ ID NO:2 and, furthermore, such sequences are well known in the art, and therefore sufficient guidance is provided to enable one of ordinary skill in the art to make and use nucleic acids encoding a protein comprising SEQ ID NO:2. Claim 4(a) is a generic claim that covers fusion proteins that comprise SEQ ID NO:2. Applicants assert that numerous species are disclosed in the specification and are well known in the art to enable the generic claim. For example, exemplary fusion and chimeric proteins, such as enzymatic fusion proteins (e.g., beta-galactosidase fusions), yeast two-hybrid GAL fusions, poly-His fusions, MYC-tagged, HI-tagged and Ig fusions, are disclosed on page 14 of the specification. Fusion proteins are useful for, for example, facilitating the purification of recombinant peptides and increasing the expression and/or secretion of a protein (e.g., by fusing a heterologous signal sequence), as discussed on page 14 of the specification. Methods of producing fusion/chimeric proteins are also described on page 14 of the specification and are well known in the art. Furthermore, the use of fusion proteins in two-hybrid systems/assays is described on pages 26-27 of the specification. In addition, production and expression of fusion proteins in fusion vectors is described on pages 51-52 of the specification. Reagents for producing and expressing fusion proteins are readily available from numerous commercial manufacturers and are well known to one of ordinary skill in the art. Thus, given the disclosure in the specification, undue experimentation would not be required by one of ordinary skill to make and use the claimed invention since a reasonable number of species are disclosed by Applicants in light of the state of the art, the skill of those in the art, the predictability of the relevant technology, etc.

Furthermore, Applicants have amended claim 4 to indicate that the claimed nucleic acid molecules encode a glucuronosyltransferase and, therefore, although the claimed nucleic acids may encode fusion/chimeric proteins having additional sequences added to SEQ ID NO:2, such additional sequences do not change the functional classification of the encoded protein as a glucuronosyltransferase.

Claim 4(b) has been amended for consistency of claim language.

Claim 4(c) has been re-written as dependent claim 30 because a sequence complementary to a nucleotide sequence of claim 4 does not encode a protein, as called for by the amended preamble of claim 4.

Rejection of claim 13 under 35 U.S.C. §112, first paragraph, 35 U.S.C. §102, and 35 U.S.C. §103

Applicants respectfully assert that claim 13 is novel, unobvious, and is supported by a written description sufficient to enable one of ordinary skill in the art to make and use the invention in a manner commensurate with the scope of the claim. However, Applicants hereby cancel claim 13, thereby making the rejection moot, in order to expedite prosecution. Cancellation of claim 13 in no way affects the scope or range of equivalents of the other pending claims, which are directed to isolated nucleic acid molecules, vectors, host cells, etc., whereas claim 13 is directed to methods of detection. Furthermore, Applicants reserve the right to pursue the material of claim 13 in a divisional application.

Conclusions

By way of the above amendments, claim 13 has been canceled; claims 4 and 24 have been amended; and claim 30 has been added. As such, claims 4, 8-9, 24, and 27-30 are currently pending.

Claims 25-26 have been allowed as indicated in the Office Action mailed September 10, 2001.

In view of the above amendments and remarks, Applicants respectfully request that the Examiner reconsider and withdraw the outstanding objections and rejections and issue a Notice of Allowance at Examiner's earliest convenience. If the Examiner wishes to discuss this response, please call Applicant's representative at the phone number below.

Respectfully submitted,
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